

1 / 3 4

SEQUENCE LISTING

<110> Oncotherapy Science, Inc.

The University of Tokyo

<120> Method of Diagnosing Breast Cancer

<130> ONC-A0306P1

<160> 34

<170> PatentIn version 3.1

<210> 1

<211> 928

<212> DNA

<213> Homo sapiens

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<222> (127).. (720)

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gggatc atg cag aga gct tca cgt ctg aag aga gag ctg cac atg tta 168

2 / 3 4

Met Gln Arg Ala Ser Arg Leu Lys Arg Glu Leu His Met Leu

1

5

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gcc aca gag cca ccc cca ggc atc aca tgt tgg caa gat aaa gac caa 216

Ala Thr Glu Pro Pro Pro Gly Ile Thr Cys Trp Gln Asp Lys Asp Gln

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atg gat gac ctg cga gct caa ata tta ggt gga gcc aac aca cct tat 264

Met Asp Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr

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gag aaa ggt gtt ttt aag cta gaa gtt atc att cct gag agg tac cca 312

Glu Lys Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro

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ttt gaa cct cct cag atc cga ttt ctc act cca att tat cat cca aac 360

Phe Glu Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn

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att gat tct gct gga agg att tgt ctg gat gtt ctc aaa ttg cca cca 408

Ile Asp Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro

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85

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aaa ggt gct tgg aga cca tcc ctc aac atc gca act gtg ttg acc tct 456

Lys Gly Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser

95

100

105

110

3 / 3 4

att cag ctg ctc atg tca gaa ccc aac cct gat gac ccg ctc atg gct 504
Ile Gln Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala
115 120 125

gac ata tcc tca gaa ttt aaa tat aat aag cca gcc ttc ctc aag aat 552
Asp Ile Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn
130 135 140

gcc aga cag tgg aca gag aag cat gca aga cag aaa caa aag gct gat 600
Ala Arg Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp
145 150 155

gag gaa gag atg ctt gat aat cta cca gag gct ggt gac tcc aga gta 648
Glu Glu Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val
160 165 170

cac aac tca aca cag aaa agg aag gcc agt cag cta gta ggc ata gaa 696
His Asn Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu
175 180 185 190

aag aaa ttt cat cct gat gtt tag gggacttgct ctggttcac ttagttaatg 750
Lys Lys Phe His Pro Asp Val
195

tggtctttgc caaggtgatc taagttgcct accttgaatt tttttttaaa tatatttgat 810

4 / 3 4

gacataattt ttgtgtagtt tatttatcctt gtacatatgt attttgaaat cttttaaacc 870

tgaaaaataa atagtcattt aatgttgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 928

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<211> 197

<212> PRT

<213> Homo sapiens

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20 25 30

Asp Leu Arg Ala Gln Ile Leu Gly Gly Ala Asn Thr Pro Tyr Glu Lys

35 40 45

Gly Val Phe Lys Leu Glu Val Ile Ile Pro Glu Arg Tyr Pro Phe Glu

5 / 3 4

50

55

60

Pro Pro Gln Ile Arg Phe Leu Thr Pro Ile Tyr His Pro Asn Ile Asp

65

70

75

80

Ser Ala Gly Arg Ile Cys Leu Asp Val Leu Lys Leu Pro Pro Lys Gly

85

90

95

Ala Trp Arg Pro Ser Leu Asn Ile Ala Thr Val Leu Thr Ser Ile Gln

100

105

110

Leu Leu Met Ser Glu Pro Asn Pro Asp Asp Pro Leu Met Ala Asp Ile

115

120

125

Ser Ser Glu Phe Lys Tyr Asn Lys Pro Ala Phe Leu Lys Asn Ala Arg

130

135

140

Gln Trp Thr Glu Lys His Ala Arg Gln Lys Gln Lys Ala Asp Glu Glu

145

150

155

160

6 / 3 4

Glu Met Leu Asp Asn Leu Pro Glu Ala Gly Asp Ser Arg Val His Asn

165

170

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Ser Thr Gln Lys Arg Lys Ala Ser Gln Leu Val Gly Ile Glu Lys Lys

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Phe His Pro Asp Val

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<222> (53).. (1189)

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Met Ser

7 / 3 4

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Gly Ala Gly Val Ala Ala Gly Thr Arg Pro Pro Ser Ser Pro Thr Pro

5

10

15

ggc tct cgg cgc cgg cgc cag cgc ccc tct gtg ggc gtc cag tcc ttg 154

Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln Ser Leu

20

25

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agg ccg cag agc ccg cag ctc agg cag agc gac ccg cag aaa cgg aac 202

Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys Arg Asn

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ctg gac ctg gag aaa agc ctg cag ttc ctg cag cag cag cac tcg gag 250

Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His Ser Glu

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atg ctg gcc aag ctc cat gag gag atc gag cat ctg aag cgg gaa aac 298

Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg Glu Asn

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75

80

aag gat ctc cat tac aag ctc ata atg aat cag aca tca cag aag aaa 346

Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln Lys Lys

85

90

95

8 / 3 4

gat ggc ccc tca gga aac cac ctt tcc agg gcc tct gct ccc ttg ggc 394
Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro Leu Gly
100 105 110

gct cgc tgg gtc tgc atc aac gga gtg tgg gta gag ccg gga gga ccc 442
Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly Gly Pro
115 120 125 130

agc cct gcc agg ctg aag gag ggc tcc tca cgg aca cac agg cca gga 490
Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg Pro Gly
135 140 145

ggc aag cgt ggg cgt ctt gcg ggc ggt agc gcc gac act gtg cgc tct 538
Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val Arg Ser
150 155 160

cct gca gac agc ctc tcc atg tca agc ttc cag tct gtc aag tcc atc 586
Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys Ser Ile
165 170 175

tct aat tca ggc aag gcc agg ccc cag ccc ggc tcc ttc aac aag caa 634
Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn Lys Gln
180 185 190

gat tca aaa gct gac gtc tcc cag aag gcg gac ctg gaa gag gag ccc 682
Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu Glu Pro

9 / 3 4

195	200	205	210	
cta ctt cac aac agc aag ctg gac aaa gtt cct ggg gta caa ggg cag				730
Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln Gly Gln				
	215	220	225	
gcc aga aag gag aaa gca gag gcc tct aat gca gga gct gcc tgt atg				778
Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala Cys Met				
	230	235	240	
ggg aac agc cag cac cag ggc agg cag atg ggg gcg ggg gca cac ccc				826
Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala His Pro				
	245	250	255	
cca atg atc ctg ccc ctt ccc ctg cga aag ccc acc aca ctt agg cag				874
Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu Arg Gln				
	260	265	270	
tgc gaa gtg ctc atc cgc gag ctg tgg aat acc aac ctc ctg cag acc				922
Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu Gln Thr				
275	280	285	290	
caa gag ctg cgg cac ctc aag tcc ctc ctg gaa ggg agc cag agg ccc				970
Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln Arg Pro				
	295	300	305	

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cag gca gcc ccg gag gaa gct agc ttt ccc agg gac caa gaa gcc acg 1018

Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu Ala Thr

310

315

320

cat ttc ccc aag gtc tcc acc aag agc ctc tcc aag aaa tgc ctg agc 1066

His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys Leu Ser

325

330

335

cca cct gtg gcg gag cgt gcc atc ctg ccc gca ctg aag cag acc ccg 1114

Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln Thr Pro

340

345

350

aag aac aac ttt gcc gag agg cag aag agg ctg cag gca atg cag aaa 1162

Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met Gln Lys

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360

365

370

cgg cgc ctg cat cgc tca gtg ctt tga gccaccccaa tctggtcagt 1209

Arg Arg Leu His Arg Ser Val Leu

375

gccaggccca ccaacctgca gctggagact ggctctctat agcatttcct gatacttcg 1269

ctacttttag gcctggctaa attccaagac agataacact caagatagat aaagtacttg 1329

atctccaaac tgacaaactg tttatattct agctgttatt ttgctatttg gcatttacat 1389

1 1 / 3 4

aaaagcacac gatgaagcag gtatgcctt acctgttgaa actgaaaata aagcttgttt 1449

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<211> 378

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<213> Homo sapiens

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Thr Pro Gly Ser Arg Arg Arg Arg Gln Arg Pro Ser Val Gly Val Gln

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Ser Leu Arg Pro Gln Ser Pro Gln Leu Arg Gln Ser Asp Pro Gln Lys

35 40 45

Arg Asn Leu Asp Leu Glu Lys Ser Leu Gln Phe Leu Gln Gln Gln His

50 55 60

1 2 / 3 4

Ser Glu Met Leu Ala Lys Leu His Glu Glu Ile Glu His Leu Lys Arg
65 70 75 80

Glu Asn Lys Asp Leu His Tyr Lys Leu Ile Met Asn Gln Thr Ser Gln
85 90 95

Lys Lys Asp Gly Pro Ser Gly Asn His Leu Ser Arg Ala Ser Ala Pro
100 105 110

Leu Gly Ala Arg Trp Val Cys Ile Asn Gly Val Trp Val Glu Pro Gly
115 120 125

Gly Pro Ser Pro Ala Arg Leu Lys Glu Gly Ser Ser Arg Thr His Arg
130 135 140

Pro Gly Gly Lys Arg Gly Arg Leu Ala Gly Gly Ser Ala Asp Thr Val
145 150 155 160

1 3 / 3 4

Arg Ser Pro Ala Asp Ser Leu Ser Met Ser Ser Phe Gln Ser Val Lys

165

170

175

Ser Ile Ser Asn Ser Gly Lys Ala Arg Pro Gln Pro Gly Ser Phe Asn

180

185

190

Lys Gln Asp Ser Lys Ala Asp Val Ser Gln Lys Ala Asp Leu Glu Glu

195

200

205

Glu Pro Leu Leu His Asn Ser Lys Leu Asp Lys Val Pro Gly Val Gln

210

215

220

Gly Gln Ala Arg Lys Glu Lys Ala Glu Ala Ser Asn Ala Gly Ala Ala

225

230

235

240

Cys Met Gly Asn Ser Gln His Gln Gly Arg Gln Met Gly Ala Gly Ala

245

250

255

His Pro Pro Met Ile Leu Pro Leu Pro Leu Arg Lys Pro Thr Thr Leu

260

265

270

1 4 / 3 4

Arg Gln Cys Glu Val Leu Ile Arg Glu Leu Trp Asn Thr Asn Leu Leu
275 280 285

Gln Thr Gln Glu Leu Arg His Leu Lys Ser Leu Leu Glu Gly Ser Gln
290 295 300

Arg Pro Gln Ala Ala Pro Glu Glu Ala Ser Phe Pro Arg Asp Gln Glu
305 310 315 320

Ala Thr His Phe Pro Lys Val Ser Thr Lys Ser Leu Ser Lys Lys Cys
325 330 335

Leu Ser Pro Pro Val Ala Glu Arg Ala Ile Leu Pro Ala Leu Lys Gln
340 345 350

Thr Pro Lys Asn Asn Phe Ala Glu Arg Gln Lys Arg Leu Gln Ala Met
355 360 365

1 5 / 3 4

Gln Lys Arg Arg Leu His Arg Ser Val Leu

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aagcgcgggt gaagcgcgca ggtcggagtg acagctgcgc tgccggccc gctgcggtca 240

gcaacgcgcc atg gac gca gag ctg gca gag gtg cgc gcc ttg caa gct 289

Met Asp Ala Glu Leu Ala Glu Val Arg Ala Leu Gln Ala

1

5

10

1 6 / 3 4

gag atc gcg gcc ctg cgg cga gcg tgt gag gac cca ccg gcg ccc tgg 337
Glu Ile Ala Ala Leu Arg Arg Ala Cys Glu Asp Pro Pro Ala Pro Trp
15 20 25

gaa gag aag tcc cga gtc caa aaa tct ttt caa gcc ata cac caa ttc 385
Glu Glu Lys Ser Arg Val Gln Lys Ser Phe Gln Ala Ile His Gln Phe
30 35 40 45

aat ttg gaa gga tgg aag tct tca aaa gat ctg aaa aat cag ctt gga 433
Asn Leu Glu Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly
50 55 60

cat tta gaa tca gaa ctt tca ttt cta agt acg ctt act ggc atc aat 481
His Leu Glu Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn
65 70 75

ata aga aat cac tcc aag cag aca gaa gac cta aca agc act gag atg 529
Ile Arg Asn His Ser Lys Gln Thr Glu Asp Leu Thr Ser Thr Glu Met
80 85 90

aca gaa aag agt att aga aaa gtt cta cag aga cac aga tta tca gga 577
Thr Glu Lys Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly
95 100 105

aat tgc cac atg gtt aca ttt caa ctt gaa ttt cag att ctg gaa att 625

17 / 34

Asn Cys His Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile

110

115

120

125

cag aat aag gag aga tta tct tct gct gtt act gac ctc aac ata ata 673

Gln Asn Lys Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile

130

135

140

atg gag ccc aca gaa tgc tca gaa tta agt gaa ttt gtg tct aga gca 721

Met Glu Pro Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala

145

150

155

gaa gag aga aaa gat ctg ttc atg ttt ttc cga agc ctg cat ttt ttt 769

Glu Glu Arg Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe

160

165

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gtg gag tgg ttt gaa tat cgt aag cgc acg ttt aaa cat ctc aag gaa 817

Val Glu Trp Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu

175

180

185

aag tac cca gat gcc gtg tac ctc tcg gag ggg ccc tcc tcc tgc tcc 865

Lys Tyr Pro Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser

190

195

200

205

atg ggg atc cgc agc gcc agc cgg cca ggg ttt gaa tta gtc att gtt 913

Met Gly Ile Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val

210

215

220

1 8 / 3 4

tgg agg ata caa ata gat gaa gat ggg aag gtt ttt cca aag ctg gat 961

Trp Arg Ile Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp

225

230

235

ctt ctc acc aaa gtc cca cag cga gcc ctg gag ctg gac aag aac aga 1009

Leu Leu Thr Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg

240

245

250

gcc ata gaa act gct cct ctc agc ttc cga acc ctg gta gga ctg ctt 1057

Ala Ile Glu Thr Ala Pro Leu Ser Phe Arg Thr Leu Val Gly Leu Leu

255

260

265

gga atc gaa gct gct ctg gaa agc ctg ata aaa tcg ctt tgt gca gag 1105

Gly Ile Glu Ala Ala Leu Glu Ser Leu Ile Lys Ser Leu Cys Ala Glu

270

275

280

285

gag aac aac tagttccaaa acagtgaacg tggaggatga agatgctgcg 1154

Glu Asn Asn

tggaggaaca tgcaatttta ttcaatataa acatttgcta ttttctgctt agaaaccaca 1214

ccctgaagac gtgctgtcta tgcagttatg gcacattata tggaaactct catgacatga 1274

aaaataaata caactagtta agtataaaat gccaaaaaaa a 1315

19 / 34

<210> 6

<211> 288

<212> PRT

<213> Homo sapiens

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Ser Arg Val Gln Lys Ser Phe Gln Ala Ile His Gln Phe Asn Leu Glu

35 40 45

Gly Trp Lys Ser Ser Lys Asp Leu Lys Asn Gln Leu Gly His Leu Glu

50 55 60

Ser Glu Leu Ser Phe Leu Ser Thr Leu Thr Gly Ile Asn Ile Arg Asn

65 . 70 . 75 80

Ser Ile Arg Lys Val Leu Gln Arg His Arg Leu Ser Gly Asn Cys His
100 105 110

Met Val Thr Phe Gln Leu Glu Phe Gln Ile Leu Glu Ile Gln Asn Lys
115 120 125

Glu Arg Leu Ser Ser Ala Val Thr Asp Leu Asn Ile Ile Met Glu Pro
130 135 140

Thr Glu Cys Ser Glu Leu Ser Glu Phe Val Ser Arg Ala Glu Glu Arg
145 150 155 160

Lys Asp Leu Phe Met Phe Phe Arg Ser Leu His Phe Phe Val Glu Trp
165 170 175

2 1 / 3 4

Phe Glu Tyr Arg Lys Arg Thr Phe Lys His Leu Lys Glu Lys Tyr Pro
180 185 190

Asp Ala Val Tyr Leu Ser Glu Gly Pro Ser Ser Cys Ser Met Gly Ile
195 200 205

Arg Ser Ala Ser Arg Pro Gly Phe Glu Leu Val Ile Val Trp Arg Ile
210 215 220

Gln Ile Asp Glu Asp Gly Lys Val Phe Pro Lys Leu Asp Leu Leu Thr
225 230 235 240

Lys Val Pro Gln Arg Ala Leu Glu Leu Asp Lys Asn Arg Ala Ile Glu
245 250 255

Thr Ala Pro Leu Ser Phe Arg Thr Leu Val Gly Leu Leu Gly Ile Glu
260 265 270

Ala Ala Leu Glu Ser Leu Ile Lys Ser Leu Cys Ala Glu Glu Asn Asn

2 2 / 3 4

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2 3 / 3 4

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<212> DNA

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<223> Artificially synthesis primer for RT-PCR

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<211> 23

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<210> 11

2 4 / 3 4

<211> 20

<212> DNA

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<210> 12

<211> 23

<212> DNA

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<223> Artificially synthesis primer for RT-PCR

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<210> 13

<211> 23

<212> DNA

2 5 / 3 4

<213> Artificial

<220>

<223> Artificially synthesis primer for RT-PCR

<400> 13

agagccatag aaactgctcc tct

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<210> 14

<211> 23

<212> DNA

<213> Artificial

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<223> Artificially synthesis primer for RT-PCR

<400> 14

cataactgca tagacagcac gtc

23

<210> 15

<211> 20

<212> DNA

<213> Artificial

2 6 / 3 4

<220>

<223> Artificially synthesis primer for RT-PCR

<400> 15

gggaagagaa gtcccgagtc

20

<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Artificially synthesis primer for RT-PCR

<400> 16

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24

<210> 17

<211> 30

<212> DNA

<213> Artificial

<220>

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27 / 34

<400> 17

caagcagtcc taccagggtt cggaagctga

30

<210> 18

<211> 30

<212> DNA

<213> Artificial

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<223> Artificially synthesis primer for Nested PCR

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30

<210> 19

<211> 30

<212> DNA

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28 / 34

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<211> 33

<212> DNA

<213> Artificial

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<223> Artificially synthesis primer for PCR

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<212> DNA

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<223> Artificially synthesis primer for PCR

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<212> DNA

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<223> Artificially synthesis primer for PCR

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30

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<212> DNA

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<223> Artificially synthesis oligonucleotides for siRNA

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51

<210> 26

<211> 51

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3 1 / 3 4

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<223> target sequence for siRNA

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gaagcagcac gacttctt 18

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<220>

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catcgcaact gtgttgacc

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<210> 32

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3 4 / 3 4

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19

<210> 34

<211> 19

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<223> target sequence for siRNA

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gtacgcttac tggcatcaa

19